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SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Philip E.Branton et al.

(ii) TITLE OF THE INVENTION: Adenovirus E4 Protein For
Inducing Cell Death

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Clark & Elbing LLP

(B) STREET: 176 Federal Street

(C) CITY: Boston

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 3 July 1997

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/021,273

(B) FILING DATE: 5 July 1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/028,740

(B) FILING DATE: 22 October 1996

(ix) ATTORNEY/AGENT INFORMATION:

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 885 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10

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ATGACTACGT CGGCGGTTC ATTGGCATG ACACTACGAC CAACACGATC TCGGTTGTCT      60
CGGCGCACTC CGTACAGTAG GGATCGTCTA CCTCCTTTTG AGACAGAAAC CCGCGCTACC      120
ATACTGGAGG ATCATCCGCT GCTGCCCGAA TGTAAACACTT TGACAATGCA CAACGTGAGT      180
TACGTGCGAG GTCTTCCCTG CAGTGTGGGA TTTACGCTGA TTCAGGAATG GGTGTGTCCC      240
TGGGATATGG TTCTAACGCG GGAGGAGCCT GTAATCCTGA GGAAGTGTAT GCACGTGTGC      300
CTGTGTTGTG CCAACATTGA TATCATGACG AGCATGATGA TCCATGGTTA CGAGTCCTGG      360
GCTCTCCACT GTCAATTGTC CAGTCCCGGT TCCCTGCAGT GTATAGCCGG CGGCGCAGTT      420
TTGGCCAGCT GGTTTAGGAT GGTGGTGGAT GCGGCCATGT TTAATCAGAG GTTTATATGG      480
TACCGGAGAG TGGTGAATTA CAACATGCCA AAGAGAGTAA TGTTTATGTC CAGCGTGTGT      540
ATGAGGGGTC GCCACTTAAT CTACCTGCGC TTGTGGTATG ATGGCCACGT GGGTTCTGTG      600
GTCCCCGCCA TGAGCTTTGG ATACAGCGCC TTGCACTGTG GGATTTTGAA CAATATTGTG      660
GTGCTGTGCT GCAGTTACTG TGCTGATTTA AGTGAGATCA GGGTGCCTG CTGTGCCCGG      720
AGGACAAGCG GCCTTATGCT GCGGGCGGTG CGAATCATCG CTGAGGAGAC CACTGCCATG      780
TTGTATTCTT CAGAGCGGGA GCGGCGCGCG CAGCAGTTTA TTCGCGCGCT GCTGCAGCAC      840
CACCGCCCTA TCTGTATGCA CGATTATGAC TCTACCCCCA TGTAG                                     885

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 294 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30

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Met Thr Thr Ser Gly Val Pro Phe Gly Met Thr Leu Arg Pro Thr Arg
  1      5      10      15
Ser Arg Leu Ser Arg Arg Thr Pro Tyr Ser Arg Asp Arg Leu Pro Pro
  20      25      30
Phe Glu Thr Glu Thr Arg Ala Thr Ile Leu Glu Asp His Pro Leu Leu
  35      40      45
Pro Glu Cys Asn Thr Leu Thr Met His Asn Val Ser Tyr Val Arg Gly
  50      55      60
Leu Pro Cys Ser Val Gly Phe Thr Leu Ile Gln Glu Trp Val Val Pro
  65      70      75      80
Trp Asp Met Val Leu Thr Arg Glu Glu Leu Val Ile Leu Arg Lys Cys
  85      90      95
Met His Val Cys Leu Cys Cys Ala Asn Ile Asp Ile Met Thr Ser Met
  100      105      110
Met Ile His Gly Tyr Glu Ser Trp Ala Leu His Cys His Cys Ser Ser
  115      120      125
Pro Gly Ser Leu Gln Cys Ile Ala Gly Gly Gln Val Leu Ala Ser Trp
  130      135      140

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Phe Arg Met Val Val Asp Gly Ala Met Phe Asn Gln Arg Phe Ile Trp
 145 150 155 160
 Tyr Arg Glu Val Val Asn Tyr Asn Met Pro Lys Glu Val Met Phe Met
 165 170 175
 5 Ser Ser Val Phe Met Arg Gly Arg His Leu Ile Tyr Leu Arg Leu Trp
 180 185 190
 Tyr Asp Gly His Val Gly Ser Val Pro Ala Met Ser Phe Gly Tyr
 195 200 205
 10 Ser Ala Leu His Cys Gly Ile Leu Asn Asn Ile Val Val Leu Cys Cys
 210 215 220
 Ser Tyr Cys Ala Asp Leu Ser Glu Ile Arg Val Arg Cys Cys Ala Arg
 225 230 235 240
 Arg Thr Arg Arg Leu Met Leu Arg Ala Val Arg Ile Ile Ala Glu Glu
 245 250 255
 15 Thr Thr Ala Met Leu Tyr Ser Cys Arg Thr Glu Arg Arg Arg Gln Gln
 260 265 270
 Phe Ile Arg Ala Leu Leu Gln His His Arg Pro Ile Leu Met His Asp
 275 280 285
 Tyr Asp Ser Thr Pro Met
 290

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTTCTTC CAGCTCTTCC CGCTCCTCCC GTGTGTGACT CGCAGAACGA ATGTGTAGGT 60
 TGGCTGGGTG TGGCTTAATC TGCGGTGGTG GATGTTATCA GGCAGCGCG GCATGAAGGA 120
 GTTACATAG AACCCGAAGC CAGGGGGCGC CTGGATGCTT TGAGAGAGTG GATATACTAC 180
 AACTACTACA CAGAGCGATC TAAGCGGCGA GACCGGAGAC GCAGATCTGT TTGTCACGCC 240
 CGCACCTGGT TTTGCTTCAG GAAATATGAC TACGTCCGGC GTTCCATTG GCATGACACT 300
 ACGACCAACA CGATCTCGGT TGCTCGGCG CACTCCGTAC AGTAG 345

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Pro Ala Leu Pro Ala Pro Pro Val Cys Asp Ser Gln Asn
 1 5 10 15

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Glu Cys Val Gly Trp Leu Gly Val Ala Tyr Ser Ala Val Val Asp Val
 20 25 30
 Ile Arg Ala Ala Ala His Glu Gly Val Tyr Ile Glu Pro Glu Ala Arg
 35 40 45
 5 Gly Arg Leu Asp Ala Leu Arg Glu Trp Ile Tyr Tyr Asn Tyr Tyr Thr
 50 55 60
 Glu Arg Ser Lys Arg Arg Asp Arg Arg Arg Ser Val Cys His Ala
 65 70 75 80
 10 Arg Thr Trp Phe Cys Phe Arg Lys Tyr Asp Tyr Val Arg Arg Ser Ile
 85 90 95
 Trp His Asp Thr Thr Thr Asn Thr Ile Ser Val Val Ser Ala His Ser
 100 105 110
 Val Gln

What is claimed is: